



RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/676,873
Source: OIPF
Date Processed by STIC: 4-8-04

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 703-308-4212; FAX: 703-308-4221

Effective 12/13/03: TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.1 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkr41note.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry directly to (EFFECTIVE 12/01/03):
U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office, Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 10/08/03

Raw Sequence Listing Error Summary

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: 10/676,873
ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE		
1 _____ Wrapped Nucleics _____ Wrapped Aminos	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."	
2 _____ Invalid Line Length	The rules require that a line not exceed 72 characters in length. This includes white spaces.	
3 _____ Misaligned Amino _____ Numbering	The numbering under each 5 th amino acid is misaligned. Do not use tab codes between numbers; use space characters , instead.	
4 _____ Non-ASCII	The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text .	
5 _____ Variable Length	Sequence(s) _____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.	
6 _____ PatentIn 2.0 _____ "bug"	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.	
7 _____ Skipped Sequences (OLD RULES)	Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence: (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading) (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) This sequence is intentionally skipped Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.	
8 _____ Skipped Sequences (NEW RULES)	Sequence(s) _____ missing. If intentional , please insert the following lines for each skipped sequence. <210> sequence id number <400> sequence id number 000	
9 _____ Use of n's or Xaa's (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing. Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.	
10 ✓ Invalid <213> _____ Response	Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence	
11 _____ Use of <220>	Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 07/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)	
12 _____ PatentIn 2.0 _____ "bug"	Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.	
13 _____ Misuse of n/Xaa	"n" can only represent a single <u>nucleotide</u> ; "Xaa" can only represent a single <u>amino acid</u>	



Does Not Comply
Corrected Diskette Needed

IFWO

RAW SEQUENCE LISTING

DATE: 04/08/2004

PATENT APPLICATION: US/10/676,873

TIME: 07:33:37

Input Set : N:\efs\i0676873_efs\COTHP01002-usbios-S000001.txt

Output Set: N:\CRF4\04082004\J676873.raw

3 <110> APPLICANT: CHAN, JOHN

4 BAYNES, BRIAN

5 ZHANG, SHENGSHENG

7 <120> TITLE OF INVENTION: METHODS OF ENGINEERING SPATIALLY CONSERVED MOTIFS IN
POLYPEPTIDES

9 <130> FILE REFERENCE: COTH-PO1-002

11 <140> CURRENT APPLICATION NUMBER: 10/676,873

12 <141> CURRENT FILING DATE: 2003-09-30

14 <150> PRIOR APPLICATION NUMBER: 60/414,688

15 <151> PRIOR FILING DATE: 2002-09-30

17 <160> NUMBER OF SEQ ID NOS: 4

19 <170> SOFTWARE: PatentIn version 3.2

21 <210> SEQ ID NO: 1

22 <211> LENGTH: 474

23 <212> TYPE: DNA

24 <213> ORGANISM: TNF alpha chain b mutation

26 <400> SEQUENCE: 1

27 gtcagatcat cttctcgaac ccgagtgac aagcctgtag cccatgttgt agcaaaccct 60
 29 caagctgagg ggcagctcca gtggctgaac cgccgggcca atgccctcct ggccaatggc 120
 31 gtggagctga gagataacca gctggtggtg ccatcagagg gcctgtacct catctactcc 180
 33 caggtcctct tcaagggccca aggctgcccc tccacccatg tgctcctcac ccacaccatc 240
 35 agccgcatcg cagtctccta ccagaccaag gtcaacctcc tctctgccat caagagcccc 300
 37 tgccagaggg agaccccaga gggggctgag gccaagccct ggtatgagcc catcgatctg 360
 39 ggaggggtct tccagctgga gaagggtgac cgactcagcg ctgagatcaa tcggcccgac 420
 41 tatctcgact ttgccgagtc tgggcaggtc tactttggga tcattgccct gtga 474

44 <210> SEQ ID NO: 2

45 <211> LENGTH: 157

46 <212> TYPE: PRT

47 <213> ORGANISM: TNF alpha protein

49 <400> SEQUENCE: 2

51 Val Arg Ser Ser Ser Arg Thr Pro Ser Asp Lys Pro Val Ala Gly Val
 52 1 5 10 15
 55 Val Ala Asn Pro Gln Ala Glu Gly Gln Leu Gln Trp Leu Asn Arg Arg
 56 20 25 30
 59 Ala Asn Ala Leu Leu Ala Asn Gly Val Glu Leu Arg Asp Asn Gln Leu
 60 35 40 45
 63 Val Val Pro Ser Glu Gly Leu Tyr Leu Ile Tyr Ser Gln Val Leu Phe
 64 50 55 60
 67 Lys Gly Gln Gly Cys Pro Ser Thr His Val Leu Thr His Thr Ile
 68 65 70 75 80
 71 Ser Arg Ile Ala Val Ser Tyr Gln Thr Lys Val Asn Leu Leu Ser Ala
 72 85 90 95
 75 Ile Lys Ser Pro Cys Gln Arg Glu Thr Pro Glu Gly Ala Glu Ala Lys
 76 100 105 110

Please see item #10 on
ERROR SUMMARY SHEET

- Same - see item #10

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79 Pro Gln Tyr Glu Pro Ile Asp Leu Gly Gly Val Phe Gln Leu Glu Lys
80 115 120 125
83 Gly Asp Arg Leu Ser Ala Glu Ile Asn Arg Pro Asp Tyr Leu Leu Phe
84 130 135 140
87 Ala Glu Ser Gly Gln Val Tyr Phe Gly Ile Ile Ala Leu
88 145 150 155
91 <210> SEQ ID NO: 3
92 <211> LENGTH: 474
93 <212> TYPE: DNA
94 <213> ORGANISM: TNF alpha chain c mutation — Same — see item #10
96 <400> SEQUENCE: 3
97 gtcagatcat cttctcgaac cccgagtgac aagcctgtag cccatgttgt agcaaaccct. 60
99 caagctgagg ggcagctcca gtggctgaac cgccgggcca atgccctcct ggccaatggc 120
101 gtggagctga gagataacca gctgggtgtg ccatcagagg gctgtacct catcagttcc 180
103 caggtcctct tcaagggcca aggctgcccc tccaccocatg tgctcctcac ccacaccatc 240
105 agccgcatcg ccgtctccta ccagaccaag gtcaacctcc tctctgccat caagagcccc 300
107 tgccagaggg agaccccaga gggggctgag gccaaagcct ggtatgagcc catccatctg 360
109 ggaggggtct tccagctgga gaagggtgac cgactcagcg ctgagatcaa tcggcccgcg 420
111 tatctcgact ttgccgagtc tgggcaggtc tactttggga tcattgccct gtga 474
114 <210> SEQ ID NO: 4
115 <211> LENGTH: 157
116 <212> TYPE: PRT
117 <213> ORGANISM: TNF alpha protein sequence chain c — same — see item #10
119 <400> SEQUENCE: 4
121 Val Arg Ser Ser Ser Arg Thr Pro Ser Asp Lys Pro Val Ala His Val
122 1 5 10 15
125 Val Ala Asn Pro Gln Ala Glu Gly Gln Leu Gln Trp Leu Asn Arg Arg
126 20 25 30
129 Ala Asn Ala Leu Leu Ala Asn Gly Val Glu Leu Arg Asp Asn Gln Leu
130 35 40 45
133 Val Val Pro Ser Glu Gly Leu Tyr Leu Ile Ser Ser Gln Val Leu Phe
134 50 55 60
137 Lys Gly Gln Gly Cys Pro Ser Thr His Val Leu Leu Thr His Thr Ile
138 65 70 75 80
141 Ser Arg Ile Ala Val Ser Tyr Gln Thr Lys Val Asn Leu Leu Ser Ala
142 85 90 95
145 Ile Lys Ser Pro Cys Gln Arg Glu Thr Pro Glu Gly Ala Glu Ala Lys
146 100 105 110
149 Pro Gln Tyr Glu Pro Ile His Leu Gly Gly Val Phe Gln Leu Glu Lys
150 115 120 125
153 Gly Asp Arg Leu Ser Ala Glu Ile Asn Arg Pro Asp Tyr Leu Leu Phe
154 130 135 140
157 Ala Glu Ser Gly Gln Val Tyr Phe Gly Ile Ile Ala Leu
158 145 150 155

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/676,873

DATE: 04/08/2004

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